

SEQUENCE LISTING

<110> LEUNG, DAVID W.
 ADOUREL, DANIEL
 HOLLENBACK, DAVID

<120> MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

<130> 077319/0275

<140> 09/970,989

<141> 2001-10-05

<150> 09/215,252

<151> 1998-12-18

<150> 08/618,651

<151> 1996-03-19

<160> 45

<170> PatentIn Ver. 2.1

<210> 1

<211> 2242

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (319)..(1167)

<400> 1

```

ggaagtcagc aggcgttggg gaggggtggc gggggaatag cggcggcagc agccccagcc 60
ctcagagaga cagcagaaag ggagggaggg aggggtgctgg ggggacagcc cccaccatt 120
cctaccgcta tgggcccaac ctccactcc cacctcccct ccatcggccg gggctaggac 180
acccccaaat cccgtcgccc ccttggcacc gacacccga cagagacaga gacacagcca 240
tccgccacca ccgctgccgc agcctggctg gggagggggc cagcccccca ggccccctac 300
ccctctgagg tggccaga atg gat ttg tgg cca ggg gca tgg atg ctg ctg 351
                Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu
                  1                5                10

ctg ctg ctc ttc ctg ctg ctg ctc ttc ctg ctg ccc acc ctg tgg ttc 399
Leu Leu Leu Phe Leu Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe
                15                20                25

tgc agc ccc agt gcc aag tac ttc ttc aag atg gcc ttc tac aat ggc 447
Cys Ser Pro Ser Ala Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly
                30                35                40

tgg atc ctc ttc ctg gct gtg ctc gcc atc cct gtg tgt gcc gtg cga 495
Trp Ile Leu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg
                45                50                55

```

gga cgc aac gtc gag aac atg aag atc ttg cgt cta atg ctg ctc cac 543
 Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg Leu Met Leu Leu His
 60 65 70 75

atc aaa tac ctg tac ggg atc cga gtg gag gtg cga ggg gct cac cac 591
 Ile Lys Tyr Leu Tyr Gly Ile Arg Val Glu Val Arg Gly Ala His His
 80 85 90

ttc cct ccc tcg cag ccc tat gtt gtt gtc tcc aac cac cag agc tct 639
 Phe Pro Pro Ser Gln Pro Tyr Val Val Val Ser Asn His Gln Ser Ser
 95 100 105

ctc gat ctg ctt ggg atg atg gag gta ctg cca ggc cgc tgt gtg ccc 687
 Leu Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg Cys Val Pro
 110 115 120

att gcc aag cgc gag cta ctg tgg gct ggc tct gcc ggg ctg gcc tgc 735
 Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys
 125 130 135

tgg ctg gca gga gtc atc ttc atc gac cgg aag cgc acg ggg gat gcc 783
 Trp Leu Ala Gly Val Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala
 140 145 150 155

atc agt gtc atg tct gag gtc gcc cag acc ctg ctc acc cag gac gtg 831
 Ile Ser Val Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val
 160 165 170

agg gtc tgg gtg ttt cct gag gga acg aga aac cac aat ggc tcc atg 879
 Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met
 175 180 185

ctg ccc ttc aaa cgt ggc gcc ttc cat ctt gca gtg cag gcc cag gtt 927
 Leu Pro Phe Lys Arg Gly Ala Phe His Leu Ala Val Gln Ala Gln Val
 190 195 200

ccc att gtc ccc ata gtc atg tcc tcc tac caa gac ttc tac tgc aag 975
 Pro Ile Val Pro Ile Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys
 205 210 215

aag gag cgt cgc ttc acc tcg gga caa tgt cag gtg cgg gtg ctg ccc 1023
 Lys Glu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro
 220 225 230 235

cca gtg ccc acg gaa ggg ctg aca cca gat gac gtc cca gct ctg gct 1071
 Pro Val Pro Thr Glu Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala
 240 245 250

gac aga gtc cgg cac tcc atg ctc act gtt ttc cgg gaa atc tcc act 1119
 Asp Arg Val Arg His Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr
 255 260 265

gat ggc cgg ggt ggt ggt gac tat ctg aag aag cct ggg ggc ggt ggg 1167
 Asp Gly Arg Gly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
 270 275 280

tgaaccctgg ctctgagctc tctctcccatc tgtcccccac tctctcccca cacctaccca 1227

cccagtgggc cctgaagcag ggccaaaccc tcttccttgt ctccccctctc cccacttatt 1287
 ctccctctttg gaatcttcaa cttctgaagt gaatgtggat acagcggcac tcttgccccc 1347
 tcttgccccc atccatggac tcttgccctcg gtgcagtttc cactcttgac cccacactcc 1407
 tactgtcttg tctgtgggac agttgcctcc ccctcatctc cagtgaactca gcctacacaa 1467
 gggaggggaa cattccatcc ccagtggagt ctcttcctat gtgggtcttct ctaccctct 1527
 acccccacat tggccagtgg actcatccat tctttggaac aaatcccccc cactccaaa 1587
 gtccatggat tcaatggact catccatttg tgaggaggac ttctcgccct ctggctggaa 1647
 gctgatacct gaagcactcc caggctcatc ctgggagctt tcctcagcac cttcaccttc 1707
 cctcccagtg tagcctcctg tcagtggggg ctggaccctt ctaattcaga ggtctcatgc 1767
 ctgcccttgc ccagatgccc agggctcgtgc actctctggg ataccagttc agtctccaca 1827
 tttctgggtt tctgtcccca tagtacagtt cttcagtgga catgaccca cccagccccc 1887
 tgcagccctg ctgaccatct caccagacac aaggggaaga agcagacatc aggtgctgca 1947
 ctcacttctg cccctggggg agttggggaa aggaacgaac cctggctgga ggggatagga 2007
 gggcttttaa tttatttctt tttctgttga ggcttcccc tctctgagcc agttttcatt 2067
 tcttcctggg ggcattagcc actccctgcc tctcactcca gacctgttcc cacaactggg 2127
 gaggtaggct gggagcaaaa ggagaggggtg ggaccagtt ttgcgtgggt ggtttttatt 2187
 aattatctgg ataacagcaa aaaaactgaa aataaagaga gagagaaaaa aaaaa 2242

<210> 2
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Asp Leu Trp Pro Gly Ala Trp Met Leu Leu Leu Leu Leu Phe Leu
 1 5 10 15
 Leu Leu Leu Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala
 20 25 30
 Lys Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu
 35 40 45
 Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu
 50 55 60
 Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr
 65 70 75 80

Gly Ile Arg Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln
 85 90 95
 Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly
 100 105 110
 Met Met Glu Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu
 115 120 125
 Leu Leu Trp Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val
 130 135 140
 Ile Phe Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser
 145 150 155 160
 Glu Val Ala Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe
 165 170 175
 Pro Glu Gly Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg
 180 185 190
 Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
 195 200 205
 Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe
 210 215 220
 Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu
 225 230 235 240
 Gly Leu Thr Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His
 245 250 255
 Ser Met Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly
 260 265 270
 Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly Gly
 275 280

<210> 3

<211> 303

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 3

Met Ser Val Ile Gly Arg Phe Leu Tyr Tyr Leu Arg Ser Val Leu Val
 1 5 10 15
 Val Leu Ala Leu Ala Gly Cys Gly Phe Tyr Gly Val Ile Ala Ser Ile
 20 25 30
 Leu Cys Thr Leu Ile Gly Lys Gln His Leu Ala Gln Trp Ile Thr Ala
 35 40 45
 Arg Cys Phe Tyr His Val Met Lys Leu Met Leu Gly Leu Asp Val Lys
 50 55 60

Val Val Gly Glu Glu Asn Leu Ala Lys Lys Pro Tyr Ile Met Ile Ala
 65 70 75 80
 Asn His Gln Ser Thr Leu Asp Ile Phe Met Leu Gly Arg Ile Phe Pro
 85 90 95
 Pro Gly Cys Thr Val Thr Ala Lys Lys Ser Leu Lys Tyr Val Pro Phe
 100 105 110
 Leu Gly Trp Phe Met Ala Leu Ser Gly Thr Tyr Phe Leu Asp Arg Ser
 115 120 125
 Lys Arg Gln Glu Ala Ile Asp Thr Leu Asn Lys Gly Leu Glu Asn Val
 130 135 140
 Lys Lys Asn Lys Arg Ala Leu Trp Val Phe Pro Glu Gly Thr Arg Ser
 145 150 155 160
 Tyr Thr Ser Glu Leu Thr Met Leu Pro Phe Lys Lys Gly Ala Phe His
 165 170 175
 Leu Ala Gln Gln Gly Lys Ile Pro Ile Val Pro Val Val Val Ser Asn
 180 185 190
 Thr Ser Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys
 195 200 205
 Met Ile Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys
 210 215 220
 Asp Lys Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met Val Asp
 225 230 235 240
 Thr Leu Lys Glu Ile Gly Tyr Ser Pro Ala Ile Asn Asp Thr Thr Leu
 245 250 255
 Pro Pro Gln Ala Ile Glu Tyr Ala Ala Leu Gln His Asp Lys Lys Val
 260 265 270
 Asn Lys Lys Ile Lys Asn Glu Pro Val Pro Ser Val Ser Ile Ser Asn
 275 280 285
 Asp Val Asn Thr His Asn Glu Gly Ser Ser Val Lys Lys Met His
 290 295 300

<210> 4

<211> 245

<212> PRT

<213> Escheria coli

<400> 4

Met Leu Tyr Ile Phe Arg Leu Ile Ile Thr Val Ile Tyr Ser Ile Leu
 1 5 10 15
 Val Cys Val Phe Gly Ser Ile Tyr Cys Leu Phe Ser Pro Arg Asn Pro
 20 25 30

Lys His Val Ala Thr Phe Gly His Met Phe Gly Arg Leu Ala Pro Leu
 35 40 45
 Phe Gly Leu Lys Val Glu Cys Arg Lys Pro Thr Asp Ala Glu Ser Tyr
 50 55 60
 Gly Asn Ala Ile Tyr Ile Ala Asn His Gln Asn Asn Tyr Asp Met Val
 65 70 75 80
 Thr Ala Ser Asn Ile Val Gln Pro Pro Thr Val Thr Val Gly Lys Lys
 85 90 95
 Ser Leu Leu Trp Ile Pro Phe Phe Gly Gln Leu Tyr Trp Leu Thr Gly
 100 105 110
 Asn Leu Leu Ile Asp Arg Asn Asn Arg Thr Lys Ala His Gly Thr Ile
 115 120 125
 Ala Glu Val Val Asn His Phe Lys Lys Arg Arg Ile Ser Ile Trp Met
 130 135 140
 Phe Pro Glu Gly Thr Arg Ser Arg Gly Arg Gly Leu Leu Pro Phe Lys
 145 150 155 160
 Thr Gly Ala Phe His Ala Ala Ile Ala Ala Gly Val Pro Ile Ile Pro
 165 170 175
 Val Cys Val Ser Thr Thr Ser Asn Lys Ile Asn Leu Asn Arg Leu His
 180 185 190
 Asn Gly Leu Val Ile Val Glu Met Leu Pro Pro Ile Asp Val Ser Gln
 195 200 205
 Tyr Gly Lys Asp Gln Val Arg Glu Leu Ala Ala His Cys Arg Ser Ile
 210 215 220
 Met Glu Gln Lys Ile Ala Glu Leu Asp Lys Glu Val Ala Glu Arg Glu
 225 230 235 240
 Ala Ala Gly Lys Val
 245

<210> 5
 <211> 374
 <212> PRT
 <213> Zea mays

<400> 5
 Met Ala Ile Pro Leu Val Leu Val Val Leu Pro Leu Gly Leu Leu Phe
 1 5 10 15
 Leu Leu Ser Gly Leu Ile Val Asn Ala Ile Gln Ala Val Leu Phe Val
 20 25 30
 Thr Ile Arg Pro Phe Ser Lys Ser Phe Tyr Arg Arg Ile Asn Arg Phe
 35 40 45

Leu Ala Glu Leu Leu Trp Leu Gln Leu Val Trp Val Val Asp Trp Trp
 50 55 60
 Ala Gly Val Lys Val Gln Leu His Ala Asp Glu Glu Thr Tyr Arg Ser
 65 70 75 80
 Met Gly Lys Glu His Ala Leu Ile Ile Ser Asn His Arg Ser Asp Ile
 85 90 95
 Asp Trp Leu Ile Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly
 100 105 110
 Ser Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile
 115 120 125
 Gly Trp Ser Met Trp Phe Ala Glu Tyr Leu Phe Leu Glu Arg Ser Trp
 130 135 140
 Ala Lys Asp Glu Lys Thr Leu Lys Trp Gly Leu Gln Arg Leu Lys Asp
 145 150 155 160
 Phe Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe
 165 170 175
 Thr Pro Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Ala Ser Gln Gly
 180 185 190
 Leu Pro Ala Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val
 195 200 205
 Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr
 210 215 220
 Thr Val Ile Val Pro Lys Asp Ser Pro Gln Pro Thr Met Leu Arg Ile
 225 230 235 240
 Leu Lys Gly Gln Ser Ser Val Ile His Val Arg Met Lys Arg His Ala
 245 250 255
 Met Ser Glu Met Pro Lys Ser Asp Glu Asp Val Ser Lys Trp Cys Lys
 260 265 270
 Asp Ile Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Leu Ala Thr
 275 280 285
 Gly Thr Phe Asp Glu Glu Ile Arg Pro Ile Gly Arg Pro Val Lys Ser
 290 295 300
 Leu Leu Val Thr Leu Phe Trp Ser Cys Leu Leu Leu Phe Gly Ala Ile
 305 310 315 320
 Glu Phe Phe Lys Trp Thr Gln Leu Leu Ser Thr Trp Arg Gly Val Ala
 325 330 335
 Phe Thr Ala Ala Gly Met Ala Leu Val Thr Gly Val Met His Val Phe
 340 345 350

Ile Met Phe Ser Gln Ala Glu Arg Ser Ser Ser Ala Arg Ala Ala Arg
 355 360 365

Asn Arg Val Lys Lys Glu
 370

<210> 6
 <211> 1383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40)..(876)

<220>
 <221> modified_base
 <222> (1127)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1134)
 <223> a, t, c, g, other or unknown

<400> 6
 ggagcgcgagct ggcgggcgcgcg tcggggcgccg ggcgggggcc atg gag ctg tgg ccg 54
 Met Glu Leu Trp Pro
 1 5

tgt ctg gcc gcg gcg ctg ctg ttg ctg ctg ctg ctg gtg cag ctg agc 102
 Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Val Gln Leu Ser
 10 15 20

cgc gcg gcc gag ttc tac gcc aag gtc gcc ctg tac tgc gcg ctg tgc 150
 Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu Tyr Cys Ala Leu Cys
 25 30 35

ttc acg gtg tcc gcc gtg gcc tcg ctc gtc tgc ctg ctg tgc cac ggc 198
 Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys Leu Leu Cys His Gly
 40 45 50

ggc cgg acg gtg gag aac atg agc atc atc ggc tgg ttc gtg cga agc 246
 Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly Trp Phe Val Arg Ser
 55 60 65

ttc aag tac ttt tac ggg ctc cgc ttc gag gtg cgg gac ccg cgc agg 294
 Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val Arg Asp Pro Arg Arg
 70 75 80 85

ctg cag gag gcc cgt ccc tgt gtc atc gtc tcc aac cac cag agc atc 342
 Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser Asn His Gln Ser Ile
 90 95 100

ctg gac atg atg ggc ctc atg gag gtc ctt ccg gag cgc tgc gtg cag 390
 Leu Asp Met Met Gly Leu Met Glu Val Leu Pro Glu Arg Cys Val Gln
 105 110 115

atc gcc aag cgg gag ctg ctc ttc ctg ggg ccc gtg ggc ctc atc atg 438
 Ile Ala Lys Arg Glu Leu Leu Phe Leu Gly Pro Val Gly Leu Ile Met
 120 125 130

tac ctc ggg ggc gtc ttc ttc atc aac cgg cag cgc tct agc act gcc 486
 Tyr Leu Gly Gly Val Phe Phe Ile Asn Arg Gln Arg Ser Ser Thr Ala
 135 140 145

atg aca gtg atg gcc gac ctg ggc gag cgc atg gtc agg gag aac ctc 534
 Met Thr Val Met Ala Asp Leu Gly Glu Arg Met Val Arg Glu Asn Leu
 150 155 160 165

aaa gtg tgg atc tat ccc gag ggt act cgc aac gac aat ggg gac ctg 582
 Lys Val Trp Ile Tyr Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu
 170 175 180

ctg cct ttt aag aag ggc gcc ttc tac ctg gca gtc cag gca cag gtg 630
 Leu Pro Phe Lys Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val
 185 190 195

ccc atc gtc ccc gtg gtg tac tct tcc ttc tcc tcc ttc tac aac acc 678
 Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr
 200 205 210

aag aag aag ttc ttc act tca gga aca gtc aca gtg cag gtg ctg gaa 726
 Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu
 215 220 225

gcc atc ccc acc agc ggc ctc act gcg gcg gac gtc cct gcg ctc gtg 774
 Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val
 230 235 240 245

gac acc tgc cac cgg gcc atg agg acc acc ttc ctc cac atc tcc aag 822
 Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser Lys
 250 255 260

acc ccc cag gag aac ggg gcc act gcg ggg tct ggc gtg cag ccg gcc 870
 Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln Pro Ala
 265 270 275

cag tag ccagaccac ggcagggcat gacctgggga gggcaggtgg aagccgatgg 926
 Gln

ctggaggatg ggcagagggg actcctcccg gcttccaaat accactctgt ccggtcccc 986

cagctctcac tcagcccggg aagcaggaag ccccttctgt cactgggtctc agacacaggc 1046

ccctgggtgtc ccctgcaggg ggctcagctg gacctcccc gggctcgagg gcagggactc 1106

gcgccccacgg cacctctggg ngctgggntg ataaagatga ggcttgccgc tgtggcccgc 1166

tggtgggctg agccacaagg ccccgatgg ccaggagca gatgggagga ccccgaggcc 1226

aggagtccca gactcacgca ccctgggcca cagggagccg ggaatcgggg cctgctgctc 1286

ctgctggcct gaagaatctg tggggtcagc actgtactcc gttgctgttt ttttataaac 1346

acactcttgg aaaaaaaaaa aaaaaaaaaa aaaaaaa

1383

<210> 7

<211> 278

<212> PRT

<213> Homo sapiens

<400> 7

Met Glu Leu Trp Pro Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu
 1 5 10 15

Leu Val Gln Leu Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu
 20 25 30

Tyr Cys Ala Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys
 35 40 45

Leu Leu Cys His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly
 50 55 60

Trp Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val
 65 70 75 80

Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser
 85 90 95

Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val Leu Pro
 100 105 110

Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Leu Phe Leu Gly Pro
 115 120 125

Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe Phe Ile Asn Arg Gln
 130 135 140

Arg Ser Ser Thr Ala Met Thr Val Met Ala Asp Leu Gly Glu Arg Met
 145 150 155 160

Val Arg Glu Asn Leu Lys Val Trp Ile Tyr Pro Glu Gly Thr Arg Asn
 165 170 175

Asp Asn Gly Asp Leu Leu Pro Phe Lys Lys Gly Ala Phe Tyr Leu Ala
 180 185 190

Val Gln Ala Gln Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser
 195 200 205

Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr
 210 215 220

Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp
 225 230 235 240

Val Pro Ala Leu Val Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe
 245 250 255

Leu His Ile Ser Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser
 260 265 270

Gly Val Gln Pro Ala Gln
 275

<210> 8

<211> 248

<212> PRT

<213> Haemophilus influenzae

<400> 8

Met Leu Lys Leu Leu Arg Ile Phe Leu Val Leu Ile Cys Cys Ile Leu
 1 5 10 15

Ile Cys Val Leu Gly Thr Ile Tyr Ser Phe Ile Arg Phe Lys Asn Pro
 20 25 30

Ser Asn Val Gly Ile Val Ala Arg Trp Phe Gly Arg Leu Phe Thr Tyr
 35 40 45

Pro Leu Phe Gly Leu Lys Val Glu His Arg Ile Pro Gln Asp Gln Lys
 50 55 60

Gln Ile Ser Arg Ala Ile Tyr Ile Gly Asn His Gln Asn Asn Tyr Asp
 65 70 75 80

Met Val Thr Ile Ser Tyr Met Val Gln Pro Arg Thr Val Ser Val Gly
 85 90 95

Lys Lys Ser Leu Ile Trp Ile Pro Phe Phe Phe Thr Gly Ile Leu Tyr
 100 105 110

Trp Val Thr Gly Asn Ile Phe Leu Asp Arg Glu Asn Arg Thr Lys Ala
 115 120 125

His Asn Thr Met Ser Gln Leu Ala Arg Arg Ile Asn Glu Asp Asn Leu
 130 135 140

Ser Ile Trp Met Phe Pro Glu Gly Thr Arg Asn Arg Gly Arg Gly Leu
 145 150 155 160

Leu Pro Phe Lys Thr Gly Ala Phe Thr Phe His Ala Ala Ile Ser Ala
 165 170 175

Gly Val Pro Ile Ile Pro Val Val Cys Ser Ser Thr His Asn Lys Ile
 180 185 190

Asn Leu Asn Arg Trp Asp Asn Gly Lys Val Ile Cys Glu Ile Met Asp
 195 200 205

Pro Ile Asp Val Ser Gly Tyr Thr Lys Asp Asn Val Arg Asp Leu Ala
 210 215 220

Ala Tyr Cys His Phe Thr Asp Leu Met Glu Lys Arg Ile Ala Glu Leu
 225 230 235 240

Asp Glu Glu Ile Ala Lys Gly Asn
245

<210> 9

<211> 253

<212> PRT

<213> Salmonella typhimurium

<400> 9

Met Leu Tyr Ile Phe Arg Leu Ile Val Thr Val Ile Tyr Ser Ile Leu
1 5 10 15

Val Cys Val Phe Gly Ser Ile Tyr Cys Leu Phe Ser Pro Arg Asn Pro
20 25 30

Lys His Val Ala Thr Phe Gly His Met Phe Gly Arg Leu Phe Thr Ala
35 40 45

Pro Leu Phe Gly Leu Lys Val Glu Cys Arg Lys Pro Ala Asp Ala Glu
50 55 60

Asn Tyr Gly Asn Ala Ile Tyr Ile Ala Asn His Gln Asn Asn Tyr Asp
65 70 75 80

Met Val Thr Ala Ala Asn Ile Val Gln Pro Pro Thr Val Thr Val Gly
85 90 95

Lys Lys Ser Leu Leu Trp Ile Pro Phe Phe Phe Thr Gly Gln Leu Tyr
100 105 110

Trp Leu Thr Gly Asn Leu Leu Ile Asp Arg Asn Asn Arg Ala Lys Ala
115 120 125

His Ser Thr Ile Ala Ala Val Val Asn His Phe Lys Lys Arg Arg Ile
130 135 140

Ser Ile Trp Met Phe Pro Glu Gly Thr Arg Ser Arg Gly Arg Gly Leu
145 150 155 160

Leu Pro Phe Lys Thr Gly Ala Phe Thr Phe His Ala Ala Ile Ala Ala
165 170 175

Gly Val Pro Ile Ile Pro Val Cys Val Ser Asn Thr Ser Asn Lys Val
180 185 190

Asn Leu Asn Arg Leu Asn Asn Gly Leu Val Ile Val Glu Met Leu Pro
195 200 205

Pro Val Asp Val Ser Glu Tyr Gly Lys Asp Gln Val Arg Glu Leu Ala
210 215 220

Ala His Cys Arg Phe Thr Ala Leu Met Glu Gln Lys Ile Ala Glu Leu
225 230 235 240

Asp Lys Glu Val Ala Glu Arg Glu Ala Thr Gly Lys Val
245 250

<400> 10

Pro Ala Val Ala Ala Thr Ala Asp Asp Asp Lys Asp Gly Val Phe Met
20 25 30

Val Leu Leu Ser Cys Phe Lys Ile Phe Val Cys Phe Ala Phe Thr Val
35 40 45

Val Leu Ile Thr Ala Val Ala Trp Gly Leu Ile Met Val Leu Leu Leu
50 55 60

Pro Trp Pro Tyr Met Arg Ile Arg Leu Gly Asn Leu Tyr Gly His Ile
65 70 75 80

Ile Gly Gly Leu Val Ile Trp Ile Tyr Gly Ile Pro Ile Lys Ile Gln
85 90 95

Gly Ser Glu His Thr Lys Lys Arg Ala Ile Phe Thr Tyr Ile Ser Asn
100 105 110

His Ala Ser Pro Ile Asp Ala Phe Phe Val Met Trp Leu Ala Pro Ile
115 120 125

Gly Thr Val Gly Val Ala Lys Lys Glu Val Ile Trp Tyr Pro Leu Leu
130 135 140

Gly Gln Leu Tyr Thr Leu Ala His His Ile Arg Ile Asp Arg Ser Asn
145 150 155 160

Pro¹Ala Ala Ala Ile Gln Ser Phe Thr Met Lys Glu Ala Val Arg Val
165 170 175

Ile Thr Glu Lys Asn Leu Ser Leu Ile Met Phe Pro Glu Gly Thr Arg
180 185 190

Ser Gly Asp Gly Arg Leu Leu Pro Phe Lys Lys Gly Phe Val His Leu
195 200 205

Ala Leu Gln Ser His Leu Pro Ile Val Pro Met Ile Leu Thr Gly Thr
210 215 220

His Leu Ala Trp Phe Thr Arg Lys Gly Thr Phe Arg Val Arg Pro Val
225 230 235 240

Pro Ile Thr Val Lys Tyr Leu Pro Pro Ile Asn Thr Asp Asp Trp Thr
245 250 255

Val Asp Lys Ile Asp Asp Tyr Val Lys Met Ile His Asp Ile Tyr Val
260 265 270

Arg Asn Leu Pro Ala Ser Gln Lys Pro Leu Gly Ser Thr Asn Arg Ser
 275 280 285

Lys

<210> 11
 <211> 318
 <212> PRT
 <213> Cocos nucifera

<400> 11
 Met Asp Ala Ser Gly Ala Ser Ser Phe Leu Arg Gly Arg Cys Leu Glu
 1 5 10 15
 Ser Cys Phe Lys Ala Ser Phe Gly Met Ser Gln Pro Lys Asp Ala Ala
 20 25 30
 Gly Gln Pro Ser Arg Arg Pro Ala Asp Ala Asp Asp Phe Phe Thr Val
 35 40 45
 Asp Asp Asp Arg Trp Ile Thr Val Ile Leu Ser Val Val Arg Ile Ala
 50 55 60
 Ala Cys Phe Leu Ser Met Met Val Thr Thr Ile Val Trp Asn Met Ile
 65 70 75 80
 Met Leu Ile Leu Leu Pro Trp Pro Tyr Ala Arg Ile Arg Gln Gly Asn
 85 90 95
 Leu Tyr Gly His Val Thr Gly Arg Met Leu Phe Thr Met Trp Ile Leu
 100 105 110
 Gly Asn Pro Ile Thr Ile Glu Gly Ser Glu Phe Ser Asn Thr Arg Ala
 115 120 125
 Ile Tyr Ile Cys Asn His Ala Ser Leu Val Asp Ile Phe Leu Ile Met
 130 135 140
 Trp Leu Ile Pro Lys Gly Thr Val Thr Ile Ala Lys Lys Glu Ile Ile
 145 150 155 160
 Trp Tyr Pro Leu Phe Gly Gln Phe Thr Leu Tyr Val Leu Ala Asn His
 165 170 175
 Gln Arg Ile Asp Arg Ser Asn Pro Ser Ala Ala Ile Glu Ser Ile Lys
 180 185 190
 Glu Val Ala Arg Ala Val Val Lys Lys Asn Leu Ser Leu Ile Ile Phe
 195 200 205
 Pro Glu Gly Thr Arg Ser Lys Thr Gly Arg Leu Leu Pro Phe Lys Lys
 210 215 220
 Gly Phe Ile His Phe Thr Ile Ala Leu Gln Thr Arg Leu Pro Ile Val
 225 230 235 240

Pro Met Val Leu Thr Gly Thr His Leu Ala Trp Arg Lys Asn Ser Leu
245 250 255

Arg Val Arg Pro Ala Pro Ile Thr Val Lys Tyr Phe Ser Pro Ile Lys
260 265 270

Thr Asp Asp Trp Glu Glu Glu Lys Ile Asn His Tyr Val Glu Met Ile
275 280 285

His Phe Thr Ala Leu Tyr Val Asp His Leu Pro Glu Ser Gln Lys Pro
290 295 300

Leu Val Ser Lys Gly Arg Asp Ala Ser Gly Arg Ser Asn Ser
305 310 315

<210> 12

<211> 1660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (184)..(1311)

<400> 12

tctatgaaac caacatacat ggcgtttgca tcacagttgg agtcagatgt gagcccgagg 60

ggcaggtgtc tggcttgtcc acccggaagc cctgaggggca gctgttccca ctggctctgc 120

tgaccttgtg ccttggacgg ctgtcctcag cgagggggccg tgcacccgct cctgagcagc 180

gcc atg ggc ctg ctg gcc ttc ctg aag acc cag ttc gtg ctg cac ctg 228
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
1 5 10 15

ctg gtc ggc ttt gtc ttc gtg gtg agt ggt ctg gtc atc aac ttc gtc 276
Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val
20 25 30

cag ctg tgc acg ctg gcg ctc tgg ccg gtc agc aag cag ctc tac cgc 324
Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg
35 40 45

cgc ctc aac tgc cgc ctc gca tac tca ctc tgg agc caa ctg gtc atg 372
Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met
50 55 60

ctg ctg gag tgg tgg tcc tgc acg gag tgt aca ctg ttc acg gac cag 420
Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln
65 70 75

gcc acg gta gag cgc ttt ggg aag gag cac gca gtc atc atc ctc aac 468
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn
80 85 90 95

cac aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc	516
His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg	
100 105 110	
ttc gga gtg ctg ggg agc tcc aag gtc ctc gct aag aag gag ctg ctc	564
Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu	
115 120 125	
tac gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc	612
Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe	
130 135 140	
tgc aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg	660
Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu	
145 150 155	
agg cgc ctg tcg gac tac ccc gag tac atg tgg ttt ctc ctg tac tgc	708
Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys	
160 165 170 175	
gag ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg	756
Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val	
180 185 190	
gcg gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg	804
Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg	
195 200 205	
acc aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca	852
Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala	
210 215 220	
gct gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc	900
Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
ctg ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg	948
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val	
240 245 250 255	
agg aga ttt cct ctg gaa gac atc ccg ctg gat gaa aag gaa gca gct	996
Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala	
260 265 270	
cag tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata	1044
Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile	
275 280 285	
tat aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg	1092
Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg	
290 295 300	
agg ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg	1140
Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
305 310 315	

tct ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct 1188
 Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro
 320 325 330 335

ctc ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga 1236
 Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly
 340 345 350

gtt cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac 1284
 Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr
 355 360 365

gga aac caa gag ttt aag aaa aag gaa taattaatgg ctgtgactga 1331
 Gly Asn Gln Glu Phe Lys Lys Glu
 370 375

acacacgcgg ccctgacggt ggtatccagt taactcaaaa ccaacacaca gaggcagga 1391

aaagacaatt agaaactatt tttcttatta actggtgact aatattaaca aaacttgagc 1451

caagagtaaaa gaattcagaa ggctgtcag gtgaagtctt cagcctccca cagcgcaggg 1511

tcccagcatc tccacgcgcg cccgtgggag gtgggtccgg ccggagagggc ctcccgcgga 1571

cgccgtctct ccagaactcc gcttccaaga gggacctttg gctgctttct ctccttaaac 1631

ttagatcaaaa ttttaaaaaa aaaaaaaaaa 1660

<210> 13

<211> 376

<212> PRT

<213> Homo sapiens

<400> 13

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
 1 5 10 15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
 20 25 30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg
 35 40 45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu
 50 55 60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
 65 70 75 80

Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His
 85 90 95

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
 100 105 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
 115 120 125

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
 130 135 140
 Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
 145 150 155 160
 Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
 165 170 175
 Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
 180 185 190
 Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
 195 200 205
 Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
 210 215 220
 Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 225 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg
 245 250 255
 Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
 260 265 270
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
 275 280 285
 Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
 290 295 300
 Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
 305 310 315 320
 Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
 325 330 335
 Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
 340 345 350
 Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
 355 360 365
 Asn Gln Glu Phe Lys Lys Lys Glu
 370 375

<210> 14
 <211> 1523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (233)..(1174)

<400> 14

cacgctggcg ctctggccgg tcagcaagca gctctaccgc cgcctcaact gccgcctcgc 60
 ctactcactc tggagcctag cacaaaacta gaagcaaccc aagcacctgt cactggagac 120
 taattatgcg gcaccatac agggaccctc tgcggccatc atggagagcc ttcattctgc 180
 ccgtacagtt ttaagcgaaa aaggaagtat acaacaaagt ccataactgg tc atg ctg 238
 Met Leu

1

ctg gag tgg tgg tcc tgc acg gag tgt aca ctg ttc acg gac cag gcc 286
 Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala
 5 10 15

acg gta gag cgc ttt ggg aag gag cac gca gtc atc atc ctc aac cac 334
 Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His
 20 25 30

aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc ttc 382
 Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe
 35 40 45 50

gga gtg ctg ggg agc tcc aag gtc ctc gct aag aag gag ctg ctc tac 430
 Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr
 55 60 65

gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc tgc 478
 Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys
 70 75 80

aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg agg 526
 Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg
 85 90 95

cgc ctg tcg gac tac ccc gag tac atg tgg ttt ctc ctg tac tgc gag 574
 Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu
 100 105 110

ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg gcg 622
 Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala
 115 120 125 130

gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg acc 670
 Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr
 135 140 145

aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca gct 718
 Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala
 150 155 160

gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc ctg 766
 Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 165 170 175

```

ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg agg 814
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg
180 185 190

aga ttt cct ctg gaa gac atc ccg ctg gat gaa aag gaa gca gct cag 862
Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
195 200 205 210

tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata tat 910
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
215 220 225

aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg agg 958
Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
230 235 240

ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg tct 1006
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
245 250 255

ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct ctc 1054
Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
260 265 270

ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga gtt 1102
Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
275 280 285 290

cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac gga 1150
Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
295 300 305

aac caa gag ttt aag aaa aag gaa taattaatgg ctgtgactga acacacgcgg 1204
Asn Gln Glu Phe Lys Lys Lys Glu
310

ccctgacggt ggtatccagt taactcaaaa ccaacacaca gagtgcagga aaagacaatt 1264

agaaactatt tttcttatta actggtgact aatattaaca aaacttgagc caagagtaaa 1324

gaattcagaa ggcctgtcag gtgaagtctt cagcctccca cagcgcaggg tcccagcatc 1384

tccacgcgcg cccgtgggag gtgggtccgg ccggagaggc ctcccgcgga cgccgtctct 1444

ccagaactcc gcttccaaga gggacctttg gctgctttct ctccttaaac ttagatcaaa 1504

ttttaaaaaa aaaaaaaaaa 1523

```

<210> 15

<211> 314

<212> PRT

<213> Homo sapiens

<400> 15

```

Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp
1 5 10 15

```

Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu
 20 25 30
 Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu
 35 40 45
 Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu
 50 55 60
 Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val
 65 70 75 80
 Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly
 85 90 95
 Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr
 100 105 110
 Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu
 115 120 125
 Val Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro
 130 135 140
 Arg Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val
 145 150 155 160
 Ala Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro
 165 170 175
 Ser Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys
 180 185 190
 Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 195 200 205
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu
 210 215 220
 Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala
 225 230 235 240
 Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu
 245 250 255
 Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser
 260 265 270
 Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe
 275 280 285
 Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser
 290 295 300
 Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu
 305 310

```
<220>  
<221> CDS  
<222> (158) .. (1291)
```

<400> 16																		
tga	accc	cagc	cgg	ctcc	atc	tcag	ctt	ctg	gttt	cta	agt	ccat	gtg	cca	aagg	ctg	cca	60
ggaaggagac gccttcctga gtctctggatc tttcttcctt ctggaaatct ttgactgtgg 120																		
gtagttatattt attttctgaat aagagcgtcc acgcac																		175
												Met	Asp	Leu	Ala	Gly	Leu	
												1						5
ctg	aag	tct	cag	ttc	ctg	tgc	cac	ctg	gtc	ttc	tgc	tac	gtc	ttt	att			223
Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val	Phe	Cys	Tyr	Val	Phe	Ile			
			10					15				20						
gcc	tca	ggg	cta	atc	atc	aac	acc	att	cag	ctc	ttc	act	ctc	ctc	ctc			271
Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu			
			25					30				35						
tgg	ccc	att	aac	aag	cag	ctc	ttc	cgg	aag	atc	aac	tgc	aga	ctg	tcc			319
Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser			
			40					45				50						
tat	tgc	atc	tca	agc	cag	ctg	gtg	atg	ctg	ctg	gag	tgg	tgg	tcg	ggc			367
Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly			
			55					60				65					70	
acg	gaa	tgc	acc	atc	ttc	acg	gac	ccg	cgc	gcc	tac	ctc	aag	tat	ggg			415
Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly			
			75					80				85						
aag	gaa	aat	gcc	atc	gtg	gtt	ctc	aac	cac	aag	ttt	gaa	att	gac	ttt			463
Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe			
			90					95				100						
ctg	tgt	ggc	tgg	agc	ctg	tcc	gaa	cgc	ttt	ggg	ctg	tta	ggg	ggc	tcc			511
Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser			
			105					110				115						
aag	gtc	ctg	gcc	aag	aaa	gag	ctg	gcc	tat	gtc	cca	att	atc	ggc	tgg			559
Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp			
			120					125				130						
atg	tgg	tac	ttc	acc	gag	atg	gtc	ttc	tgt	tcg	cgc	aag	tgg	gag	cag			607
Met	Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln			
			135					140				145					150	
gat	cgc	aag	acg	gtt	gcc	acc	agt	ttg	cag	cac	ctc	cgg	gac	tac	ccc			655
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	Pro			
			155					160				165						

gag aag tat ttt ttc ctg att cac tgt gag ggc aca cgg ttc acg gag	703
Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu	
170 175 180	
aag aag cat gag atc agc atg cag gtg gcc cgg gcc aag ggg ctg cct	751
Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro	
185 190 195	
cgc ctc aag cat cac ctg ttg cca cga acc aag ggc ttc gcc atc acc	799
Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr	
200 205 210	
gtg agg agc ttg aga aat gta gtt tca gct gta tat gac tgt aca ctc	847
Val Arg Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu	
215 220 225 230	
aat ttc aga aat aat gaa aat cca aca ctg ctg gga gtc cta aac gga	895
Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
aag aaa tac cat gca gat ttg tat gtt agg agg atc cca ctg gaa gac	943
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu Asp	
250 255 260	
atc cct gaa gac gat gac gag tgc tgc gcc tgg ctg cac aag ctc tac	991
Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys Leu Tyr	
265 270 275	
cag gag aag gat gcc ttt cag gag gag tac tac agg acg ggc acc ttc	1039
Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr Gly Thr Phe	
280 285 290	
cca gag acg ccc atg gtg ccc ccc cgg cgg ccc tgg acc ctc gtg aac	1087
Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp Thr Leu Val Asn	
295 300 305 310	
tgg ctg ttt tgg gcc tcg ctg gtg ctc tac cct ttc ttc cag ttc ctg	1135
Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu	
315 320 325	
gtc agc atg atc agg agc ggg tct tcc ctg acg ctg gcc agc ttc atc	1183
Val Ser Met Ile Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile	
330 335 340	
ctc gtc ttc ttt gtg gcc tcc gtg gga gtt cga tgg atg att ggt gtg	1231
Leu Val Phe Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val	
345 350 355	
acg gaa att gac aag ggc tct gcc tac ggc aac tct gac agc aag cag	1279
Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln	
360 365 370	
aaa ctg aat gac tgactcaggg aggtgtcacc atccgaaggg aaccttgggg	1331
Lys Leu Asn Asp	
375	
aactgggtggc ctctgcatat cctccttagt gggacacggt gacaaaggct ggggtgagccc	1391

ctgctgggca cggcggaagt cagcacctct ccagccaggg agtctggtct caaggccgga 1451
 tggggaggaa gatgttttgt aatctttttt tccccatgtg ctttagtggg ctttggtttt 1511
 ctttttgtgc gagtgtgtgt gagaatggct gtgtggtgag tgtgaacttt gttctgtgat 1571
 catagaaagg gtatttttagg ctgcagggga gggcagggt ggggaccgaa ggggacaagt 1631
 tcccccttca tcctttggtg ctgagttttc tgtaaccctt gggtgccaga gataaagtga 1691
 aaagtgcctt aggtgagatg actaaattat gcctccaaga aaaaaaatt aaagtgcctt 1751
 tctgggtcaa aaaaaaaaaa aaa 1774

<210> 17

<211> 378

<212> PRT

<213> Homo sapiens

<400> 17

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val
1				5					10					15	
Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln
			20					25					30		
Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys
		35					40					45			
Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu
	50					55					60				
Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg
65					70					75				80	
Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His
			85						90					95	
Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg	Phe
		100						105					110		
Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr
	115						120					125			
Val	Pro	Ile	Ile	Gly	Trp	Met	Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys
	130					135					140				
Ser	Arg	Lys	Trp	Glu	Gln	Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln
145					150					155				160	
His	Leu	Arg	Asp	Tyr	Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu
			165						170					175	
Gly	Thr	Arg	Phe	Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala
		180						185					190		

Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
 195 200 205
 Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala
 210 215 220
 Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
 225 230 235 240
 Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
 245 250 255
 Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
 260 265 270
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
 275 280 285
 Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
 290 295 300
 Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
 305 310 315 320
 Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
 325 330 335
 Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
 340 345 350
 Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
 355 360 365
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp
 370 375

<210> 18

<211> 52

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Pro Phe Lys Lys Gly Ala Phe His Leu Ala Gln Gln Gly Lys Ile Pro
 1 5 10 15
 Ile Val Pro Val Val Val Ser Asn Thr Ser Thr Leu Val Ser Pro Lys
 20 25 30
 Tyr Gly Val Phe Asn Arg Gly Cys Met Ile Val Arg Ile Leu Lys Pro
 35 40 45
 Ile Ser Thr Glu
 50

<210> 19
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 19
 Pro Ser Asn Cys Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro
 1 5 10 15
 Ile Val Pro Ile Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys
 20 25 30
 Glu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro
 35 40 45
 Val Pro Thr Glu
 50

<210> 20
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 20
 tgcaagatgg aaggcgcc

18

<210> 21
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 21
 Gly Ala Phe His Leu Ala
 1 5

<210> 22
 <211> 60
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 22
 Gln Gln Gly Lys Ile Pro Ile Val Pro Val Val Val Ser Asn Thr Ser
 1 5 10 15
 Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys Met Ile
 20 25 30
 Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys Asp Lys
 35 40 45

Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met
 50 55 60

<210> 23
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 23
 Val Arg Glu Asn Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser
 1 5 10 15
 Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr
 20 25 30
 Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp
 35 40 45
 Val Pro Ala Leu Arg Gly Thr Pro Ala Thr Gly Pro
 50 55 60

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 24
 cctcaaagtg tggatctatc

20

<210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 25
 ggaagagtac accacgggga c

21

<210> 26
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
gactctagcc taggcttttg c

21

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
ctagcttata atacgactca c

21

<210> 28
<211> 23
<212> PRT
<213> Zea mays

<400> 28
Gly Leu Gln Arg Leu Lys Asp Phe Pro Arg Pro Phe Trp Leu Ala Leu
1 5 10 15
Phe Val Glu Gly Thr Arg Phe
20

<210> 29
<211> 23
<212> PRT
<213> Homo sapiens

<400> 29
Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu
1 5 10 15
Tyr Cys Glu Gly Thr Arg Phe
20

<210> 30
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 30
gactaccccg agtacatgtg gtttctc

27

<210> 31
<211> 9

<212> PRT
 <213> Homo sapiens

<400> 31
 Asp Tyr Pro Glu Tyr Met Trp Phe Leu
 1 5

<210> 32
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 32
 cacatgtccg cctcgtactt cttc

24

<210> 33
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu
 1 5 10 15
 Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln
 20 25 30
 Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr
 35 40 45

<210> 34
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
 1 5 10 15
 Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln
 20 25 30
 Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe
 35 40 45

<210> 35
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ggctctagat attaatagta atcaattac 29

<210> 36
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
cctcacgcat gcaccatggt aatagc. 26

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
ggtgcatgcg tgaggctccg gtgc 24

<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
gtagttttca cggtacctga aatggaag 28

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
ggcccggtag catgggcctg ctggccttcc 30

<210> 40
<211> 33

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 40
 taactcctcg agttattcct tttctttaa ctc

33

<210> 41
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 41
 atggtggtac caccatggac ctgcggggac tgctg

35

<210> 42
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 42
 ggaggatattc tagaggccac cagttc

26

<210> 43
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 6X-His tag

<400> 43
 His His His His His His
 1 5

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 44
cacatgtccg cctcgtactt ctte

24

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
gactctagcc taggcttttg c

21